



IFWO

RAW SEQUENCE LISTING

DATE: 10/08/2004

PATENT APPLICATION: US/10/727,358

TIME: 15:45:53

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10082004\J727358.raw

3 <110> APPLICANT: Memorial Sloan-Kettering Cancer Center
 4 Kolesnick, Richard N.
 5 Xing, Hong-Mei R.
 7 <120> TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS
 MEDIATED
 8 TUMORIGENESIS
 W--> 9 <130> FILE REFERENCE: 1216-1-006CIP
 11 <140> CURRENT APPLICATION NUMBER: US 10/727,358
 12 <141> CURRENT FILING DATE: 2003-12-03
 14 <150> PRIOR APPLICATION NUMBER: 60/384,228
 15 <151> PRIOR FILING DATE: 2002-05-30
 17 <150> PRIOR APPLICATION NUMBER: 60/460,023
 18 <151> PRIOR FILING DATE: 2003-04-03
 20 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
 21 <151> PRIOR FILING DATE: 2003-05-29
 23 <160> NUMBER OF SEQ ID NOS: 38
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 120
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 1
 33 ctgcagaagc tcatcgatat ctccatcggc agtctgcgcg ggctgcgcac caagtgtca 60
 35 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac 120
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 41
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Homo sapiens
 43 <400> SEQUENCE: 2
 45 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
 46 1 5 10 15
 49 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
 50 20 25 30
 53 Leu Glu Ala Lys Leu Val Lys Tyr Ile
 54 35 40
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 19
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Homo sapiens
 62 <400> SEQUENCE: 3
 63 ggcagtctgc gcgggctgc 19
 66 <210> SEQ ID NO: 4
 67 <211> LENGTH: 18
 68 <212> TYPE: DNA

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69 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 4
72 tcagtgtcta acgacctc                                     18
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 18
77 <212> TYPE: DNA
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 5
81 cggaccctag aggcaaag                                     18
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85 <211> LENGTH: 19
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: antisense oligonucleotide
92 <400> SEQUENCE: 6
93 cagcccgcgc agactgccg                                     19
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 18
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: antisense oligonucleotide
104 <400> SEQUENCE: 7
105 gaggtcggtta gacactga                                     18
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109 <211> LENGTH: 16
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: antisense oligonucleotide
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121 <211> LENGTH: 873
122 <212> TYPE: PRT
123 <213> ORGANISM: Mus musculus
125 <400> SEQUENCE: 9
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128 1          5          10          15
131 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
132          20          25          30
135 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
136          35          40          45
139 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
140          50          55          60
143 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
144 65          70          75          80
147 Tyr Ile Cys Lys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp

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148		85		90		95
151	Arg Thr Ala Glu	Leu Asn Ser Tyr	Pro Arg Phe Ser Asp	Trp Leu Tyr		
152		100	105		110	
155	Ile Phe Asn Val	Arg Pro Glu Val	Gln Glu Ile Pro	Gln Glu Leu		
156		115	120		125	
159	Thr Leu Asp Ala	Leu Leu Glu Met	Asp Glu Ala Lys	Ala Lys Glu Met		
160		130	135		140	
163	Leu Arg Arg Trp	Gly Ala Ser Thr	Glu Glu Cys Ser	Arg Leu Gln Gln		
164	145		150		155	160
167	Ala Leu Thr Cys	Leu Arg Lys Val	Thr Gly Leu Gly	Gly Glu His Lys		
168		165	170		175	
171	Met Asp Ser Gly	Trp Ser Ser Thr	Asp Ala Arg Asp	Ser Ser Leu Gly		
172		180	185		190	
175	Pro Pro Met Asp	Met Leu Ser Ser	Leu Gly Arg Ala	Gly Ala Ser Thr		
176		195	200		205	
179	Gln Gly Pro Arg	Ser Ile Ser Val	Ser Ala Leu Pro	Ala Ser Asp Ser		
180		210	215		220	
183	Pro Val Pro Gly	Leu Ser Glu Gly	Leu Ser Asp Ser	Cys Ile Pro Leu		
184	225		230		235	240
187	His Thr Ser Gly	Arg Leu Thr Pro	Arg Ala Leu His	Ser Phe Ile Thr		
188		245	250		255	
191	Pro Pro Thr Thr	Pro Gln Leu Arg	Arg His Ala Lys	Leu Lys Pro Pro		
192		260	265		270	
195	Arg Thr Pro Pro	Pro Pro Ser Arg	Lys Val Phe Gln	Leu Leu Pro Ser		
196		275	280		285	
199	Phe Pro Thr Leu	Thr Arg Ser Lys	Ser His Glu Ser	Gln Leu Gly Asn		
200		290	295		300	
203	Arg Ile Asp Asp	Val Thr Pro Met	Lys Phe Glu Leu	Pro His Gly Ser		
204	305		310		315	320
207	Pro Gln Leu Val	Arg Arg Asp Ile	Gly Leu Ser Val	Thr His Arg Phe		
208		325	330		335	
211	Ser Thr Lys Ser	Trp Leu Ser Gln	Val Cys Asn Val	Cys Gln Lys Ser		
212		340	345		350	
215	Met Ile Phe Gly	Val Lys Cys Lys	His Cys Arg Leu	Lys Cys His Asn		
216		355	360		365	
219	Lys Cys Thr Lys	Glu Ala Pro Ala	Cys Arg Ile Thr	Phe Leu Pro Leu		
220		370	375		380	
223	Ala Arg Leu Arg	Arg Thr Glu Ser	Val Pro Ser Asp	Ile Asn Asn Pro		
224	385		390		395	400
227	Val Asp Arg Ala	Ala Glu Pro His	Phe Gly Thr Leu	Pro Lys Ala Leu		
228		405	410		415	
231	Thr Lys Lys Glu	His Pro Pro Ala	Met Asn Leu Asp	Ser Ser Ser Asn		
232		420	425		430	
235	Pro Ser Ser Thr	Thr Ser Ser Thr	Pro Ser Ser Pro	Ala Pro Phe Leu		
236		435	440		445	
239	Thr Ser Ser Asn	Pro Ser Ser Ala	Thr Thr Pro Pro	Asn Pro Ser Pro		
240		450	455		460	
243	Gly Gln Arg Asp	Ser Arg Phe Ser	Phe Pro Asp Ile	Ser Ala Cys Ser		
244	465		470		475	480

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247 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp
248           485           490           495
251 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
252           500           505           510
255 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
256           515           520           525
259 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
260           530           535           540
263 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
264 545           550           555           560
267 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
268           565           570           575
271 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
272           580           585           590
275 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
276           595           600           605
279 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
280           610           615           620
283 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
284 625           630           635           640
287 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
288           645           650           655
291 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
292           660           665           670
295 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
296           675           680           685
299 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
300           690           695           700
303 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
304 705           710           715           720
307 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
308           725           730           735
311 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
312           740           745           750
315 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
316           755           760           765
319 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
320           770           775           780
323 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
324 785           790           795           800
327 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
328           805           810           815
331 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
332           820           825           830
335 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
336           835           840           845
339 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
340           850           855           860
343 Thr Leu Glu Ser Gly Asn Pro Lys Met

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344 865                               870
347 <210> SEQ ID NO: 10
348 <211> LENGTH: 866
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 10
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355 1                               5                               10                               15
358 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
359                               20                               25                               30
362 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
363                               35                               40                               45
366 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
367                               50                               55                               60
370 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
371 65                               70                               75                               80
374 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
375                               85                               90                               95
378 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
379                               100                              105                              110
382 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
383                               115                              120                              125
386 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
387                               130                              135                              140
390 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
391 145                              150                              155                              160
394 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
395                               165                              170                              175
398 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
399                               180                              185                              190
402 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
403                               195                              200                              205
406 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
407                               210                              215                              220
410 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
411 225                              230                              235                              240
414 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
415                               245                              250                              255
418 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
419                               260                              265                              270
422 Lys Pro Pro Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
423                               275                              280                              285
426 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
427                               290                              295                              300
430 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
431 305                              310                              315                              320
434 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
435                               325                              330                              335
438 His Arg Phe Ser Thr Lys Ser Trp Leu Ser Gln Val Cys His Val Cys

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VERIFICATION SUMMARY

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